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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lau, Lester F.

(ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
(B) STREET: 6300 Sears Tower, 233 South Wacker Drive
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: United States of America
(F) ZIP: 60606-6402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Clough, David W.
(B) REGISTRATION NUMBER: 36,107
(C) REFERENCE/DOCKET NUMBER: 28758/33766

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312/474-6300
(B) TELEFAX: 312/474-0448
(C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 180..1316

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTEC GGGCGCATTT GATCCCGCTG	120

CTCGCCGGCT	TGTTGGTTCT	GTGTCGCCGC	GCTCGCCCCG	GTTCCCTCTG	CGCGCCACA	179												
ATG	AGC	TCC	AGC	ACC	TTC	AGG	ACG	CTC	GCT	GTC	GCC	GTC	ACC	CTT	CTC		227	
Met	Ser	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu		
1					5				10						15			
CAC	TTG	ACC	AGA	CTG	GCG	CTC	TCC	ACC	TGC	CCC	GCC	GCC	TGC	CAC	TGC		275	
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys			
20					25					30								
CCT	CTG	GAG	GCA	CCC	AAG	TGC	GCC	CCG	GGA	GTC	GGG	TTG	GTC	CGG	GAC		323	
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp			
35					40					45								
GGC	TGC	GGC	TGC	TGT	AAG	GTC	TGC	GCT	AAA	CAA	CTC	AAC	GAG	GAC	TGC		371	
Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys			
50					55					60								
AGC	AAA	ACT	CAG	CCC	TGC	GAC	CAC	ACC	AAG	GGG	TTG	GAA	TGC	AAT	TTC		419	
Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe			
65					70					75					80			
GGC	GCC	AGC	TCC	ACC	GCT	CTG	AAA	GGG	ATC	TGC	AGA	GCT	CAG	TCA	GAA		467	
Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu			
85					90					95								
GGC	AGA	CCC	TGT	GAA	TAT	AAC	TCC	AGA	ATC	TAC	CAA	AAC	GGG	GAA	AGC		515	
Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser			
100					105					110								
TTC	CAG	CCC	AAC	TGT	AAA	CAC	CAG	TGC	ACA	TGT	ATT	GAT	GGC	GCC	GTG		563	
Phe	Gln	Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val			
115					120					125								
GGC	TGC	ATT	CCT	CTG	TGT	CCC	CAA	GAA	CTG	TCT	CTC	CCC	AAT	CTG	GGC		611	
Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly			
130					135					140								
TGT	CCC	AAC	CCC	CGG	CTG	GTG	AAA	GTC	AGC	GGG	CAG	TGC	TGT	GAA	GAG		659	
Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Ser	Gly	Gln	Cys	Cys	Glu	Glu			
145					150					155					160			
TGG	GTT	TGT	GAT	GAA	GAC	AGC	ATT	AAG	GAC	TGC	CTG	GAC	GAC	CAG	GAT		707	
Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Ser	Leu	Asp	Asp	Gln	Asp			
165					170					175								
GAC	CTC	CTC	GGA	CTC	GAT	GCC	TCG	GAG	GTG	GAG	TTA	ACG	AGA	AAC	AAT		755	
Asp	Leu	Leu	Gly	Leu	Asp	Ala	Ser	Glu	Val	Glu	Leu	Thr	Arg	Asn	Asn			
180					185					190								
GAG	TTA	ATC	GCA	ATT	GGA	AAA	GGC	AGC	TCA	CTG	AAG	AGG	CTT	CCT	GTC		803	
Glu	Leu	Ile	Ala	Ile	Gly	Lys	Gly	Ser	Ser	Leu	Lys	Arg	Leu	Pro	Val			
195					200					205								
TTT	GGC	ACC	GAA	CCG	CGA	GTT	CTT	TTC	AAC	CCT	CTG	CAC	GCC	CAT	GGC		851	
Phe	Gly	Thr	Glu	Pro	Arg	Val	Leu	Phe	Asn	Pro	Leu	His	Ala	His	Gly			
210					215					220								
CAG	AAA	TGC	ATC	GTT	CAG	ACC	ACG	TCT	TGG	TCC	CAG	TGC	TCC	AAG	AGC		899	
Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser			
225					230					235					240			
TGC	GGA	ACT	GGC	ATC	TCC	ACA	CGA	GTT	ACC	AAT	GAC	AAC	CCA	GAG	TGC		947	

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys			
245	250	255	
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA		995	
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln			
260	265	270	
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG		1043	
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys			
275	280	285	
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC		1091	
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val			
290	295	300	
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC		1139	
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys			
305	310	315	320
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA		1187	
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu			
325	330	335	
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA		1235	
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys			
340	345	350	
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC		1283	
Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr			
355	360	365	
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCC		1336	
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
370	375		
AGTGTGGCTT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG		1396	
AATGGTGCCTT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAACTGCC AAGGGGCTGA		1456	
TGTGGACCGA CAGCAGCGCA GCCG		1480	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
 1 5 10 15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
 20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp

35	40	45	
Gly Cys Gly Cys Cys-Lys Val Cys Ala Lys Gln-Leu Asn Glu-Asp Cys			
50	55	60	
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe			
65	70	75	80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu			
85	90	95	
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser			
100	105	110	
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val			
115	120	125	
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly			
130	135	140	
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu			
145	150	155	160
Trp-Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp			
165	170	175	
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn			
180	185	190	
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val			
195	200	205	
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly			
210	215	220	
Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser			
225	230	235	240
Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys			
245	250	255	
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln			
260	265	270	
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys			
275	280	285	
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val			
290	295	300	
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys			
305	310	315	320
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu			
325	330	335	
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys			
340	345	350	
Cys Asn Tyr. Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr			
355	360	365	
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp			

370

375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGGCC ACCCGCGACAC CGCGCCGCCA CCCCCACCCC GCTGCGCACG GCCTGTCCGC	60
TGCACACCAAG CTITGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	168
1 5 10 15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC Leu His Leu Thr Arg Leu Ala Ser Thr Cys Pro Ala Ala Cys His	216
20 25 30	
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg	264
35 40 45	
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp	312
50 55 60	
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn	360
65 70 75	
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser	408
80 85 90 95	
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu	456
100 105 110	
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala	504
115 120 125	
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu	552
130 135 140	
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG	600

Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu			
145	150	155	
GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG			648
Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln			
160	165	170	175
GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG			696
Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu			
180	185	190	
TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG			744
Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu			
195	200	205	
AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT			792
Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro			
210	215	220	
TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC			840
Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys			
225	230	235	
TCA AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC			888
Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn			
240	245	250	255
CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT			936
Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro			
260	265	270	
TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC			984
Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser			
275	280	285	
AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT			1032
Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys			
290	295	300	
TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC			1080
Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp			
305	310	315	
GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC			1128
Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe			
320	325	330	335
CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG			1176
Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln			
340	345	350	
TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT			1224
Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe			
355	360	365	
CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC			1266
Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
370	375	380	
TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT			1326
CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA			1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
 1 5 10 15

His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
 20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
 35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
 100 105 110

Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
 115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
 145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
 165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
 180 185 190

Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
 195 200 205

Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
 210 215 220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
 225 230 235 240

Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro

245	250	255	
Glu Cys Arg Leu Val Lys Glu Thr-Arg-Ile Cys Glu Val Arg Pro Cys			
260	265	270	
Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys			
275	280	285	
Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu			
290	295	300	
Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly			
305	310	315	320
Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg			
325	330	335	
Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser			
340	345	350	
Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro			
355	360	365	
Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
370	375	380	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC GACAACCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCC	60
CTGTCCGAAT CCAGGCTCCA GCCGCGCCTC TCGTCGCCCTC TGCAACCTGTC TGTGCATCCT	120
CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCGTTGGTGC	180
TCCTCGCCCT CTGCACCCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCAAGTGC	240
CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT	300
GCTGCCGCGT CTGCGCCAAG CAGCTGGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC	360
CACACAAGGG CCTCTTCTGC GATTTGGCT CCCCCGCCAA CCGCAAGATT GGAGTGTGCA	420
CTGCCAAAGA TGGTGCACCC TGTGTCITCG GTGGGTCGGT GTACCGCAGC GGTGAGTCCT	480
TCCAAAGCAG CTGCAAATAC CAATGCACTT GCCTGGATGG GGCGTGGGC TGCCTGCC	540
TATGCAGCAT GGACGTGCGC CTGCCCAGCC CTGACTGCC CTTCCCGAGA AGGGTCAAGC	600
TGCCTGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG	660

GGCCCTGCCCT AGCTGCCTAC CGACTGGAAG ACACATTTGG CCCAGACCCA ACTATGATGC	720
GAGCCAAGTG CCTGGTCCAG ACCACAGAGT GGAGCGCTG TTCTAAGACC TGTGGAATGG	780
GCATCTCCAC CCGAGTTTACCA ATGACAATA CCTTCTGCAG ACTGGAGAAG CAGAGCCGCC	840
TCTGCATGGT CAGGCCCTGC GAAGCTGACC TGGAGGAAAA CATTAAGAAG GGCAAAAAGT	900
GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTGAGCTTCTGGC TGCAACCAGTG	960
TGAAGACATA CAGGGCTAAG TTCTGCAGGG TGTGCACAGA CGGCCGCTGC TGCAACACCGC	1020
ACAGAACAC CACTCTGCCA GTGGAGTTCA AATGCCCGA TGGCGAGATC ATGAAAAAGA	1080
ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAACAGT TCCTGGGGAC AATGACATCT	1140
TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG	1200
ACACGAACCTC ATTAGACTAT AACTTGAACG GAGTTGCATC TCATTTCTT CTGTAAAAAC	1260
AATTACAGTA GCACATTAAT TAAATCTGT GTTTTTAACT ACCGTGGGAG GAACTATCCC	1320
ACCAAAGTGA GAACGTTATG TCATGGCCAT ACAAGTAGTC TGTCAACCTC AGACACTGGT	1380
TTCGAGACAG TTTACACTTG ACAGTTGTTCA ATTAGCCAC AGTGCAGAA CGCACACTGA	1440
GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT	1500
TATTTTAAAAA GCAGCAGTGT GCCTACTTT TGGAGTGTAA CCGGGGAGGG AAATTATAGC	1560
ATGCTTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCTCCAC TAGATGAGGC	1620
TGAGTCCAGC TGTTCTTAA GAACAGCACT TTCAGCCTCT GACCATTCTG ATTCCAGTGA	1680
CACTTGTCAAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTG	1740
CCTGTAACAA GCCAGATTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA	1800
TATATTGTA CAGTTATCTA AGTAAATTAA AAGTCATTG TTTTGTTTT AAGTGCTTT	1860
GGGATTTAA ACTGATAGCC TCAAACCTCA AACACCATAG GTAGGACACG AAGCTTATCT	1920
GTGATTCAAA ACAAAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCA	1980
AACAAACAAA TGCTGTGCAG GTGATAAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA	2040
AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTAT TAAGAAATGG CTGGCTCAGG	2100
GTAAGGTCCG ATTCCCTACCA GGAAGTGCTT GCTGCTCTT TGATTATGAC TGGTTGGGG	2160
TGGGGGGAG TTTATTTGTT GAGAGTGTGA CCAAAAGTTA CATGTTTGCA CCTTTCTAGT	2220
TGAAAAATAAA GTATATATAT ATTTTTATA TGAAAAAAA GGAATTC	2267

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
 1 5 10 15

Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
 20 25 30

Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
 35 40 45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50 55 60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
 65 70 75 80

Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
 85 90 95

Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
 100 105 110

Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
 115 120 125

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
 130 135 140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
 145 150 155 160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
 165 170 175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
 180 185 190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
 195 200 205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
 210 215 220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
 225 230 235 240

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
 245 250 255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
 260 265 270

Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
 275 280 285

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu Phe
 290 295 300

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys
 305 310 315 320
 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
 325 330 335
 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2075 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGGCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCGGCCACCG CGCCCTCCGC TCCGCCCCGCA	120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCGGCG TCGCCCTTCGT GGTCCCTCCTC	180
GCCCTCTGCA GCCGGCCGGC CGTGGGCCAG AACTGCAGCG GGCGGTGCCG GTGCCCCGGAC	240
GAGCCGGCGC CGCGCTGCCG GGCAGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC	300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCCGCAC	360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC	420
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACG GCAGCGGAGA GTCCCTTCCAG	480
AGCAGCTGCA AGTACCACTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC	540
AGCATGGACG TTCTGCTGCC CAGCCCTGAC TGCCCCCTTCC CGAGGAGGGT CAAGCTGCC	600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTTGGGCCT	660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCAG ACCCAACTAT GATTAGAGCC	720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC	780
TCCACCCGGG TTACCAATGA CAACGCCCTCC TGCAGGCTAG AGAACAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCAACCC TGCCGGTGGG GTTCAAGTGC CCTGACGGCG AGGTCAATGAA GAAGAACATG	1080
ATGTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA	1140

TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACTT GAACTGATTG ACATCTCATT TTTCCGTAAA AATGATTTCAT	1260
GTAGCACAG TTATTTAAAT CTGTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAACT ACATTAGTAC ACAGCACCAAG AATGTATATT AAGGTGTGGC	1440
TTTGGGAGCA GTGGGAGGGT ACCGGCCCGG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAG	1620
GTTGTCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTGAA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAAA TTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTGTGTGCC TTTTTATTTT	1860
TGTTTTAAAT GCTTTGATAT TTCAATGTTA GCCTCAATTCTGAAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCTGCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTGGCA	2040
GGCTGATTTC TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu
1					5				10					15	
Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
					20				25				30		
Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
					35				40				45		
Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
					50				55				60		
Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
					65				70				75		80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85 90 95
 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100 105 110
 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115 120 125
 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130 135 140
 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145 150 155 160
 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165 170 175
 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180 185 190
 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195 200 205
 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210 215 220
 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225 230 235 240
 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245 250 255
 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260 265 270
 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275 280 285
 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu
 290 295 300
 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305 310 315 320
 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325 330 335
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340 345

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
GGGGATCTGT GACCGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
GGGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp
1				5					10					15	
Cys	Ser	Lys	Thr	Thr	Gln										
				20											

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	Gly	Cys
1					5				10				15		
Ile	Pro	Leu	Cys	Pro											
		20													

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser	Cys	Gly
1					5			10					15		
Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr								
		20													

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys	Arg	Leu	Val	Lys
1				5					10					15	
Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro	Leu	Gln
1				5				10					15		
Thr	Arg	Thr	Val	Lys											
			20												

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